

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	2799	85.6		620	11	O70550	070550 mus musculus
2	2576.5	78.8		623	11	O88560	O88560 mus musculus
3	1672.5	51.1		619	4	Q9Y2P4	Q9Y2P4 homo sapien
4	1452	44.4		690	4	Q9Y2P5	Q9Y2P5 homo sapien
5	1379	42.2		662	11	O88694	O88694 mus musculus
6	1365	41.7		690	11	Q9ES38	Q9es38 rattus norv
7	1327.5	40.6		614	11	O88561	O88561 mus musculus
8	1051	32.1		671	5	Q9W1V9	Q9w1v9 drosophila
9	1026	31.4		661	5	Q9W185	Q9w185 drosophila
10	983.5	30.1		690	5	Q9VKU1	Q9vkul drosophila
11	958	29.3		650	5	Q19878	Q19878 caenorhabdi
12	953	29.1		608	2	Q9HZV4	Q9hzv4 pseudomonas
13	944	28.9		597	2	O05307	O05307 mycobacteri
14	937	28.6		641	4	Q95186	Q95186 homo sapien
15	936	28.6		655	5	Q18916	Q18916 caenorhabdi
16	927.5	28.4		506	11	O88562	O88562 mus musculus
17	913.5	27.9		643	3	O42633	O42633 cochllobolu
18	774.5	23.7		669	3	O60021	O60021 saccharomyc
19	398.5	12.2		502	2	O53551	O53551 mycobacteri

Db 121 WLGLLVKLGCPMACLNINIRAKSLLHCFQCCGAKVLLASPDLOEAEEALPTLKDDAVSVF 180  
Qy 181 YVSRNTDGDIDSLDKVDENSTPEIPESWRSEVTFSPALYIYTSGTGLPKAAMITHQ 240  
Db 181 YVSRNTDGDIDSLDKVDENSTPEIPESWRSEVTFSPALYIYTSGTGLPKAAMITHQ 240  
Qy 241 RIWYGTGLTFVSGLKADDDV-IYITLPHYSAALLIGHGCIIVAGATLALR-TKFSASQFWD 300  
Db 241 RIWYGTGLTFVSGLKADDDV-IYITLPHYSAALLIGHGCIIVAGATLALR-TKFSASQFWD 300  
Qy 301 CRKYNVTVIQYIGELLRYLNCSPQPNDRDHKVRALNGLRGDVMRQFVKRFGDICIYE 360  
Db 301 CRKYNVTVIQYIGELLRYLNCSPQPNDRDHKVRALNGLRGDVMRQFVKRFGDICIYE 360  
Qy 361 FYAATGNIQYIGELLRYLNCSPQPNDRDHKVRALNGLRGDVMRQFVKRFGDICIYE 420  
Db 361 FYAATGNIQYIGELLRYLNCSPQPNDRDHKVRALNGLRGDVMRQFVKRFGDICIYE 420  
Qy 421 EVGLLVCKITQITLTPFNGYAGAKAQTEKKKLRDVFVKKGLDYFNNSGDLMLMDRENFIYF 480  
Db 421 EVGLLVCKITQITLTPFNGYAGAKAQTEKKKLRDVFVKKGLDYFNNSGDLMLMDRENFIYF 480  
Qy 481 VGDTPRKNGENVAATEVADIVGLVDFVEEVNVIYGVHPDHEGRIGMASIKKENHEF 540  
Db 481 VGDTPRKNGENVAATEVADIVGLVDFVEEVNVIYGVHPDHEGRIGMASIKKENHEF 540  
Qy 541 KLFQHIADYLPSPYARPRFLRIQDTIETGTGFKHRKMTLVEEGFNPAVTKDALYFLDDTAK 600  
Db 541 KLFQHIADYLPSPYARPRFLRIQDTIETGTGFKHRKMTLVEEGFNPAVTKDALYFLDDTAK 600  
Qy 601 MYVPMTEIYNAISAKTLK 620  
Db 601 TEVPMTEIYNAISAKTLK 620

RESULT 2  
O88560 PRELIMINARY; PRT; 623 AA.  
ID O88560  
AC O88560  
DT 01-NOV-1998 (TREMELrel. 08, Created)  
DT 01-NOV-1998 (TREMELrel. 08, Last sequence update)  
DT 01-MAY-2000 (TREMELrel. 13, Last annotation update)  
DE FATTY ACID TRANSPORT PROTEIN 2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98337965; PubMed=9671728;  
RA Hirsch D., Stahl A., Lodish H.F.;  
RT "A family of fatty acid transporters conserved from mycobacterium to man."  
RL Proc. Natl. Acad. Sci. U.S.A. 95:8625-8629(1998).  
DR EMBL: AF072757; AAC40186.1;  
DR InterPro: IPR000873;  
DR Pfam: PF00501; AMP-binding; 1.  
DR PROSITE: PS00455; AMP\_BINDING; 1.  
SQ SEQUENCE 623 AA; 70594 MW; 81CC62831384E127 CRC64;

Query Match 78.8%; Score 2576.5; DB 11; Length 623;  
Best Local Similarity 77.4%; Pred. No. 1.4e-185;  
Matches 482; Conservative 54; Mismatches 84; Indels 3; Gaps 3;  
Qy 1 MLSAIYTVLAGLFLPLLVNLCOPYFFQDYGIVFLKVAAGVRRVRSYQRRPARTILRAF 60  
Db 1 MLPLVYGLAGLFLPLLVNLCOPYFFQDYGIVFLKVAAGVRRVRSYQRRPARTILRAF 60  
Qy 61 EKARQTPHPPFLFRDRETLTYAQVDRRSNOVARALHDHGLRGQDCVALLMGNEPAYVWL 120  
Db 61 EQARKTPHPPFLFRDRETLTYAQVDRRSNOVARALHDHGLRGQDCVALLMGNEPAYVWI 120

Qy 121 WLGLLVKLGCPMACLNINIRAKSLLHCFQCCGAKVLLVSPLOAAVEEILPSLKDDVSIY 180  
Db 121 WLGLLVKLGCPMACLNINIRAKSLLHCFQCCGAKVLLVSPLOAAVEEILPSLKDDVSIY 180  
Qy 181 YVSRNTDGDIDSLDKVDENSTPEIPESWRSEVTFSPALYIYTSGTGLPKAAMITHQ 240  
Db 181 YVSRNTDGDIDSLDKVDENSTPEIPESWRSEVTFSPALYIYTSGTGLPKAAMITHQ 240  
Qy 241 RIWYGTGLTFVSGLKADDDV-IYITLPHYSAALLIGHGCIIVAGATLALR-TKFSASQFWD 298  
Db 241 RIWYGTGLTFVSGLKADDDV-IYITLPHYSAALLIGHGCIIVAGATLALR-TKFSASQFWD 298  
Qy 298 DD-CRKYNTVVIQYIGELLRYLNCSPQPNDRDHKVRALNGLRGDVMRQFVKRFGDICI 357  
Db 298 DD-CRKYNTVVIQYIGELLRYLNCSPQPNDRDHKVRALNGLRGDVMRQFVKRFGDICI 357  
Qy 357 IYEFYATGNIQYIGELLRYLNCSPQPNDRDHKVRALNGLRGDVMRQFVKRFGDICI 417  
Db 357 IYEFYATGNIQYIGELLRYLNCSPQPNDRDHKVRALNGLRGDVMRQFVKRFGDICI 417  
Qy 417 PKGEVGLLVCKITQITLTPFNGYAGAKAQTEKKKLRDVFVKKGLDYFNNSGDLMLMDRENFIYF 477  
Db 417 PKGEVGLLVCKITQITLTPFNGYAGAKAQTEKKKLRDVFVKKGLDYFNNSGDLMLMDRENFIYF 477  
Qy 477 HDRVGDTPRKNGENVAATEVADIVGLVDFVEEVNVIYGVHPDHEGRIGMASIKKENHEF 537  
Db 477 HDRVGDTPRKNGENVAATEVADIVGLVDFVEEVNVIYGVHPDHEGRIGMASIKKENHEF 537  
Qy 537 DKKLFQHIADYLPSPYARPRFLRIQDTIETGTGFKHRKMTLVEEGFNPAVTKDALYFLDD 597  
Db 537 DKKLFQHIADYLPSPYARPRFLRIQDTIETGTGFKHRKMTLVEEGFNPAVTKDALYFLDD 597  
Qy 597 TAKMYVPMTEIYNAISAKTLK 620  
Db 597 TAKMYVPMTEIYNAISAKTLK 620

RESULT 3  
Q9Y2P4 PRELIMINARY; PRT; 619 AA.  
ID Q9Y2P4  
AC Q9Y2P4  
DT 01-NOV-1999 (TREMELrel. 12, Created)  
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)  
DT 01-MAR-2001 (TREMELrel. 16, Last annotation update)  
DE VERY LONG-CHAIN ACYL-COA SYNTHETASE HOMOLOG 1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX Steinberg S.J., Watkins P.A.;  
RA "Human Very Long-Chain Acyl-CoA Synthetase Homolog 1."  
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF064254; AAD29443.1;  
DR InterPro: IPR000873;  
DR Pfam: PF00501; AMP-binding; 1.  
DR PROSITE: PS00455; AMP\_BINDING; 1.  
SQ SEQUENCE 619 AA; 70111 MW; 20264CE3FBB44FF5 CRC64;

Query Match 51.1%; Score 1672.5; DB 4; Length 619;  
Best Local Similarity 50.7%; Pred. No. 1.5e-117;  
Matches 315; Conservative 116; Mismatches 187; Indels 3; Gaps 3;  
Qy 1 MLSAIYTVLAGLFLPLLVNLCOPYFFQDYGIVFLKVAAGVRRVRSYQRRPARTILRAF 59  
Db 1 MLLSWLVLAGVAGVVLVHFLQKLLFPYFDDDFWFLKVVLLIIRLKYKRGELVTLDFK 60  
Qy 60 LEKARQTPHPPFLFRDRETLTYAQVDRRSNOVARALHDHGLRGQDCVALLMGNEPAYVW 119  
Db 60 LSHAKRQPRKPFIIYEGDIYTDVDRKRSRVAHVLFNHSLSKKGDTVALLMNEPDPFVH 120

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QY 120 LNLGLVKGACACLNINIRAKSLHHCFOCCGAKVLLVSPQLAAVEEILPSLKDDVSI 179
Db 121 VWFGLAKGCVAFNLNTINRSNLLNCRACGRPALVVGADLGTVEEILPSL-SENISV 179
QY 180 YYVSRSTNTDGDIDFSDKVDVSTPEIPESWRSEVTFSTPALYIYTSGTGLPKAAAMITH 239
Db 180 WGM-KDSVPQGVISLKEKLSSTPDEVPVRSHVSVLLSKTCLYIFSGTGLPKAAVISQ 238
QY 240 QRIWYGTGLFVSLKADDDVYITLPHYHSAALLIGHGIVAGATLALTRKFSASQFWD 299
Db 239 LQVLRGSAVLWAFGCTAHDIVITLPHYHSSAAILGSGCVELGATCVLKKKFSASQFWS 298
QY 300 DCRKYNVTQYIGELLRLCNLSPQPNDRDHKVRALGNLGRDVMROFVKREGDICIY 359
Db 299 DCKKYDVTQYIGELCRYLCKOSKEGKDHKVRALGNLGRDVMROFVKREGDICIY 358
QY 360 EYAAATGNTGFMNARKYKAGVGRVNYLQKIITYDLIKYDEKDEPVRDENGICVVRPK 419
Db 359 ELYAAATGNTGFMNARKYKAGVGRVNYLQKIITYDLIKYDEKDEPVRDENGICVVRPK 418
QY 420 GEVGLLVCKITQITPENGAGAKAOTEKKLRDVFVQVNVYGVHVPDHEGRIGMASIKMKNHEFDG 539
Db 419 GEPGLLSIRVNAKNPFFGAGPYKHTKDKLLCDVFKKGDVYLTGDLIVQDDNFYFWD 478
QY 480 RVGDTFRKNGENVATTEVADTVGLVDFVQVNVYGVHVPDHEGRIGMASIKMKNHEFDG 539
Db 479 RTGDTFRKNGENVATTEVADTVGLVDFVQVNVYGVHVPDHEGRIGMASIKMKNHEFDG 538
QY 540 KLUFOHADIYPSYAPRFLRIQDTTIEITCTFKHRKMTLVEEGFNPAVKDLYFLDDTAKM 599
Db 539 EKVEQVWTFPLPAYACPRFLRIQDTTIEITCTFKHRKMTLVEEGFNPAVKDLYFLDDTAKM 598
QY 600 KATVPMTEIYNAISAKTLKL 620
Db 599 KSYVLLTRELVDQIMLGEIKL 619

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RESULT 4
QY2P5 PRELIMINARY; PRT; 690 AA.
AC QY2P5;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE VERY LONG-CHAIN ACYL-COA SYNTHETASE HOMOLOG 2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Steinberg S.J., Wang S.J., Watkins P.A.;
RT "Human Very Long-Chain Acyl-CoA Synthetase Homolog 2.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF064255; AAD29444.1;
DR InterPro; IPR000873;
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP_BINDING; 1.
SQ SEQUENCE 690 AA; 75384 MW; 011313424D794546 CRC64;

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Query Match
Best Local Similarity 44.4%; Score 1452; DB 4; Length 690;
Matches 279; Conservative 127; Mismatches 193; Indels 20; Gaps 4;
QY 11 GLFLPLLVNLCCPYFFQDIGVFLKVAAGVRRVSYGRRPARTLILAFLEKARQTPHKP 70
Db 83 GLRWLP-----ADVFLAKILHLKIRCLSRQPPDFVDFERRARQAPGGA 131
QY 71 FLIFRDE---TLTYAQVDRRSNQARALHDHIG-----LRQSGVALLMGNEPAY--VWLW 121
Db 132 LLVWTGPGAGSVTFGELARACQAALWALKAEGLGDPASLCAGEPTALLVLAQVAPALCW 191

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QY 122 LGLVKGACACLNINIRAKSLHHCFOCCGAKVLLVSPQLAAVEEILPSLKDDVSIY 181
Db 192 LGLAKLIGCTAPNINPHGRMPLAHSVLSSGARVLVVDPLRESLEEILPKLAENIRCFY 251
QY 182 VSRSTNTDGDIDFSDKVDVSTPEIPESWRSEVTFSTPALYIYTSGTGLPKAAAMITHOR 241
Db 252 LSHTSFTPGVAGALGAALDAAPSHVPADLRAGITWRSFALFYTSGTGLPKPAILTHER 311
QY 242 TWYGTGLTFVSLKADDDVYITLPHYHSAALLIGHGIVAGATLALTRKFSASQFWD 301
Db 312 VLQMSKMLSLSGATADDVVYVPLPHYHVMGLVGLGCLDGLGATCVLAPKESTSCFWD 371
QY 302 RKNYNTVQYIGELLRLCNLSPQPNDRDHKVRALGNLGRDVMROFVKREGDICIYEF 361
Db 372 RQHGVTYVQYIGELLRLCNLSPQPNDRDHKVRALGNLGRDVMROFVKREGDICIYEF 431
QY 362 YAAATGNTGFMNARKYKAGVGRVNYLQKIITYDLIKYDEKDEPVRDENGICVVRPK 421
Db 432 YGSTEGLNGLVNYVGRGALGMSCLLRLMSPFELVDFMDAAEPVRDNGFCIPVLGE 491
QY 422 VGLLVCKITQITPENGAGAKAOTEKKLRDVFVQVNVYGVHVPDHEGRIGMASIKMKNHEFD 481
Db 492 PGLLTKVVSQOPFGYGRPRELSEKLRVNRQSGDYYNTGDLVMDREGFLYFRDLR 551
QY 482 GDTFRKNGENVATTEVADTVGLVDFVQVNVYGVHVPDHEGRIGMASIKMKNHEFDGKK 541
Db 552 GDTFRKNGENVSTHEVEGLVQVDFLQVNVYGVCPGCEGKGMVAAVQLAPGQTDEK 611
QY 542 LFOHTADIYPSYAPRFLRIQDTTIEITCTFKHRKMTLVEEGFNPAVKDLYFLDDTAKM 601
Db 612 LYQHVRAWLPAYATPHFIRIQDAMEVSTFKMLKTRLVREGFNVGIVDFLVLDNRQS 671
QY 602 YVPMTEDIYNAISAKTLKL 620
Db 672 FRPLTAEMYQAVCEGTWRL 690

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RESULT 5
O88694 PRELIMINARY; PRT; 662 AA.
AC O88694;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-AUG-1999 (TREMBLrel. 11, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE FATTY ACID TRANSPORT PROTEIN 5 PRECURSOR (FATP5) (LONG-CHAIN FATTY
DE ACID TRANSPORT PROTEIN 5) (VERY-LONG-CHAIN ACYL-COA SYNTHETASE RELATED
DE PROTEIN)
ON SLC27A5 OR VLCSR.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337965; PubMed=9671728;
RA Hirsch D., Stahl A., Lodish H.F.;
RT "A family of fatty acid transporters conserved from mycobacterium to
RT man.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8625-8629(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=LIVER;
RX MEDLINE=98308102; PubMed=9642112;
RA Berger J., Truppe C., Neumann H., Forss-Petter S.;
RT "A novel relative of the very-long-chain acyl-CoA synthetase and fatty
RT acid transporter protein genes with a distinct expression pattern.";
RL Biochem. Biophys. Res. Commun. 247:255-260(1998).
CC -1- FUNCTION: INVOLVED IN TRANSLLOCATION OF LONG-CHAIN FATTY ACIDS
CC ACROSS THE PLASMA MEMBRANE. MAY PLAY A PIVOTAL ROLE IN REGULATING
CC AVAILABLE LONG-CHAIN FATTY ACID SUBSTRATES FROM EXOGENOUS SOURCES
CC IN TISSUES UNDERGOING HIGH LEVELS OF BETA-OXIDATION OR
CC TRIGLYCERIDE SYNTHESIS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PLASMA MEMBRANE.

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CC -1- TISSUE SPECIFICITY: LIVER, BUT NOT IN FETAL LIVER. LOW LEVELS IN  
 CC BRAIN, LUNG, TESTES, SPLEEN, AND SKELETAL MUSCLE.  
 CC -1- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT  
 CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.  
 DR ENBL; AF072760; AAC40189.1; -.  
 DR EMBL; AJ223959; CAAL1688.1; ALT\_INIT.  
 DR MGD; MGI:1347100; SLG2785.  
 DR InterPro; IPR000873; -.  
 DR Pfam; PF00501; AMP-binding; 1.  
 DR PROSITE; PS00455; AMP-binding; 1.  
 KW Glycoprotein; Lipid transport; Transmembrane; Signal; Transport.  
 FT SIGNAL 1 26 POTENTIAL.  
 FT CHAIN 27 662 FATTY ACID TRANSPORT PROTEIN 5.  
 FT TRANSMEM 28 48 POTENTIAL.  
 FT TRANSMEM 156 176 POTENTIAL.  
 FT TRANSMEM 312 332 POTENTIAL.  
 FT CARBOHYD 533 533 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CONFLICT 1 1 M -> MGWKKLTLLLLLLVGLGQPPWPRAM (IN  
 FT REF. 2).  
 FT CONFLICT 61 61 K -> I (IN REF. 2).  
 FT CONFLICT 381 381 T -> N (IN REF. 2).  
 FT CONFLICT 541 541 C -> S (IN REF. 2).  
 FT CONFLICT 661 661 N -> K (IN REF. 2).  
 SQ SEQUENCE 662 AA; 73251 MW; 1D7BAFE29F6D2712 CRC64;

Query Match 42.2%; Score 1379; DB 11; Length 662;  
 Best Local Similarity 42.0%; Pred. No. 2.2e-95;  
 Matches 264; Conservative 136; Mismatches 218; Indels 10; Gaps 3;

QY 2 LSALYIVLAGLLPLLLVNLCCPYFFQDYGFLKVAAGRRVRSYQORPARTILRAFLE 61  
 DB 36 LSLVGAALT-LFLLPLQPPPLGLKWLHKDVAFTKMLFYGLKFRRLNKHPPTFVDALER 94  
 QY 62 KAROTHPKPELL---FDETLTAAQVDRRSNOVARALHDHL-----GLRQDCVALLMG 112  
 DB 95 QALAWPDRVALVCTGSESSITNSQLDARSQAAVLAALKAKLDVAQNTQDAALILVLP 154  
 QY 113 NEPAYVWLGLVGLKGCAMACLNINRAKSLHCFQCCAKVLLVSPLOQAAVEILP 172  
 DB 155 KTISALSVFLGLAKGLCPVAMINPHSRGMPLLLHSSRSSGASVLIVDPDLQENLEELPK 214  
 QY 173 KDDVSYIYVSRSTNTDIDSLDKVDVSTPEIPESRSEVTFSPALYITSGTGLP 232  
 DB 215 LAENICFYLGHSPTGVEALCASIDAAPSDVPASLRATKWKSPALYITSGTGLP 274  
 QY 233 KAAMITHQRIWYGTGLTFVSGLKADDDVYITLFFYHSAALLIGIHGCIIVAGATLALRTKF 292  
 DB 275 KPAILSHERVIOQSVNLISFCGRADDDVYVLYHTIGLVGLGCLQVATCVLAPKF 334  
 QY 293 SASQFDDCKRYNTVIOYIGELLRYLCHNSPKPNDPDKHVRALNGLRGDVGWQFVKR 352  
 DB 335 SASRFAECRQHGVTVILYVGEILRYLCHNVPQEPDKIHTVRLAMGTGLRANVKNFOOR 394  
 QY 353 FGDCIYEFYAATEGNIFGMNARKVAGVGRVNLQKKIITVDLIKDYDEKDEPVRDENG 412  
 DB 395 FGPRLWEFGSTEGNVLNMGVCHGAVGRISCLRLMTPPELVQFDIETAEPLRDKG 454  
 QY 413 YCVRVPKGEVGLVCKITQITLTPFNAGAKAQAQTEKKLRDVKKGLDYFNPSGDLMLVD 472  
 DB 455 FCIPVEPGKPLLTKVRKNOPPLGYRGSAENRKLAVANRRVGDLYENTGDLVTLQDE 514  
 QY 473 NFIFYHDRVCDTRFKGENVATTEVADTVGLVDFOEVNNGVYGVHPDHEGRIGMASIKMK 532  
 DB 515 GFYFQDRLDGDTFRWKGENVSTGEVCEVLSSDLFEVNNGVYGVPGCGEKVGAAMVLA 574  
 QY 533 ENEFQCKLFOHADIYLPYARPRFLRIQDTIEITGTFKRWKMTLVEEGFNPAVKDAL 592  
 DB 575 PGKTFGQKLYQVRSWLPAYATPHFIRIQDSLEITNTKLYKSLRVREGDFVGIADPL 634  
 QY 593 YFLDDTAKMYPVMTEDIYNAISAKTLK 620  
 DB 635 YILDNKAQTFRSLMPDVOYQAVCEGTWNL 662

## RESULT 6

Q9ES38 PRELIMINARY; PRT; 690 AA.  
 ID Q9ES38  
 AC Q9ES38;  
 DT 01-MAR-2001 (TReMBLrel. 16, Created)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
 DE BILE ACID COA LIGASE  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPRAIN-SPRAQUE-DAWLEY;  
 RA Falany C.N., Xie X., Wheeler J., Wang J., Barnes S.;  
 RT "Molecular cloning and expression of rat liver bile acid CoA ligase."  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF242189; AAG09770.1; -.  
 KW Ligase.  
 SQ SEQUENCE 690 AA; 76265 MW; D5BEB8317758DA59 CRC64;

Query Match 41.7%; Score 1365; DB 11; Length 690;  
 Best Local Similarity 41.3%; Pred. No. 2.6e-94;  
 Matches 267; Conservative 134; Mismatches 212; Indels 34; Gaps 5;

QY 8 VLAGLLFL-----PLLNVNLCCP-----YFFQDYGFLKVAAGRR 42  
 DB 44 VLLGLAFGRWISSWIPHWLSLAAALTLSPRPPELRLWLDKDVAFKLLFYGLN 103  
 QY 43 VRSYQRRPARTILRAFLEKARQTPHPFLFLRDE---TLTYAQVDRRSNOVARALHDHL 99  
 DB 104 LRRRLNRPPELFVDALDAQQAARPDQVALVCTGSECSITNRELNAKACAAWALKAKL 163  
 QY 100 --GLRQD---CVALLMGNEPAYVWLGLVGLKGCAMACLNINRAKSLHCFQCCAK 153  
 DB 164 KEATIQEDKGATILVLPKSKISALSFLGLAKLGCPCVAMINPHSRGMPLLLHSSVSSGAS 223  
 QY 154 VLLVSPLEQAAVEELPLSKKDDVSYIYVSRSTNTDIDSLDKVDVSTPEIPESRSE 213  
 DB 224 VLIIVDPDLQENLEELVPLKLAENIRCFYLGHSPTGVEALGAALDAAPSDVPKALRAN 283  
 QY 214 VTFSTPALYITSGTGLPKAAMITHQRIWYGTGLTFVSGLKADDDVYITLFFYHSAALL 273  
 DB 284 IKWKSALFYITSGTGLPKAILSHERVIOQSVNLISFCGRADDDVYVNLPLVHSMGLV 343  
 QY 274 IGIHGCIVAGATLALRTKFSASQFDDCKRYNTVIOYIGELLRYLCHNSPKPNDPDKH 333  
 DB 344 LGVLGCLQGLGATCVLAPKFSASRYWAECRQYSVTVVLVYGEVLRVLCNVPGQPEDKHTV 403  
 QY 334 RLALGNLGRDVRQFVKRFGDICIYEFYAATEGNIFGMNARKVAGVGRVNLQKKIIT 393  
 DB 404 RFALGNGLRADVWENFQRFQFGPIQIWEILYSGTEGNVGLMNYVGHGAVGTSCFIRMLTP 463  
 QY 394 YDLIKDYDEKDEPVRDENGICVVRPKGEVGLVCKITQITLTPFNAGAKAQAQTEKKLRDV 453  
 DB 464 LELVQFDIETAEPRVQKQFCIPVETGKPGLLTKIRKNQPLFGYRGSDQETKRKLAVN 523  
 QY 454 FKKGDLVFNSGDLMLVDHENFIYPHDRVGDTRFKGENVATTEVADTVGLVDFOEVNNGV 513  
 DB 524 RQVGLDLYNTGDVVALQOEGFFYFRDLRGDTFRWKGENVSTREVEGVLSILDFLEEVN 583  
 QY 514 GVHPDHEGRIGMASIKMENHEPDKGLKQHIADYLPYARPRFLRIQDTIEITGTFKH 573  
 DB 584 GVTVPCEGKGVGAAMVLAAPKGTEDGQKLYQVRSWLPAYATPHFIRIQDSLEITNTYKL 643  
 QY 574 RKMTLVEEGFNPAVKDALYFLDDTAKMYPVMTEDIYNAISAKTLK 620  
 DB 644 VKSQLAREGDFVGIADPLYLIDNKAETFRSLMPDVOYQAVCEGTWNL 690

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RESULT 7
O88561 ID O88561 PRELIMINARY; PRT; 614 AA.
AC O88561;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FATTY ACID TRANSPORT PROTEIN 3 (FATP3) (LONG-CHAIN FATTY ACID
DE TRANSPORT PROTEIN 3) (FRAGMENT).
GN SLC27A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337965; PubMed=96711728;
RA Hirsch D., Stahl A., Lodish H.F.;
RT "A family of fatty acid transporters conserved from mycobacterium to
man.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8625-8629(1998).
CC -1- FUNCTION: INVOLVED IN TRANSLLOCATION OF LONG-CHAIN FATTY ACIDS
CC ACROSS THE PLASMA MEMBRANE. MAY PLAY A PIVOTAL ROLE IN REGULATING
CC AVAILABLE LONG-CHAIN FATTY ACID SUBSTRATES FROM EXOGENOUS SOURCES
CC IN TISSUES UNDERGOING HIGH LEVELS OF BETA-OXIDATION OR
CC TRIGLYCERIDE SYNTHESIS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PLASMA MEMBRANE.
CC -1- TISSUE SPECIFICITY: LUNG, LIVER, AND TESTIS.
CC -1- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT
CC COVALENT BINDING OF AMP TO THEIR SUBSTRATE.
DR EMBL; AF072758; AAC40187.1; -
DR MGD; MGI:1347358; SLC27a3.
DR InterPro; IPR000873; -
DR Pfam; PF00501; AMP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00455; AMP_BINDING; 1.
KW Glycoprotein; Lipid transport; Transmembrane; Transport.
FT NON_TER 1 1
FT TRANSMEM 99 119 POTENTIAL.
FT TRANSMEM 262 282 POTENTIAL.
FT CARBOHYD 367 367 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 614 AA; 67041 MW; 33C2A558CDD9D989 CRC64;

Query Match 40.6%; Score 1327.5; DB 11; Length 614;
Best Local Similarity 43.0%; Pred. No. 1.4e-91;
Matches 255; Conservative 107; Mismatches 196; Indels 35; Gaps 1;

QY 63 ARQTHPKFLLFRDFTLYAQVDRSRNOVARALHDHLG----- 100
DB 22 AREQTHFTFLINGAQRFSYAEARESNRIARAFLRARWGTGRRGSGRSTEGARVAPP 81
QY 101 -----LRQDCVALLMGNPEAYVWLHLGLVKLCMACLNINRAKSLHLCF 147
DB 82 AGDAAARTTAPPLAGATVALLPAGDPFLWIFGLAKAGLRTAFPTALRRGLHLCL 141
QY 148 QCCGAKVLLSPQLAAVEEILPSLKDDVSIYVSRSTNTDGDIDSLDKVDVSTPEIP 207
DB 142 RSCGASALVLAATEFLESLEPDLPALRANGLHLWATGETNVAGISNLLSEADQVDEPVP 201
QY 208 ESWRSEVFTSPALYITSTGTLPLKAMITHQRIWGTGLTFVSGLKADDDVIYITLPFY 267
DB 202 GYLSAPQNMIDTCLYITSTGTLPLKARISHLVKLVLCQGFYHLCGVHQEDVIYLAFLY 261
QY 268 HSAALLIGHICIVAGATLALTRFSAQFQWDCRKYNNVTYVIGELLYRLCNSPKPN 327
DB 262 HMSGSLGIVCGLGATVVLKPFSAQFQWDCQKHRTVTFVIGELCYLVNQPPSKA 321
QY 328 DRDHVKVRLALNGLRGDVWQFVKRFGDICIYEFYAAATEGNIGPMYARKVAGRVNYL 387
DB 322 EFDHKVRLAVGSLRPDWTWERFLRFGPLQLIETYGTEGNVATFNTYTGQAVGRASWL 381

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QY 388 OKKIITYDLIKYDEKDEPVRDENGVCYVRPKGEVGLLVCKITQITPFGNGYAGAKAOTEK 447
DB 382 YKHIFPFSILRYDVTGEPINRAQHCMTTSPGEPGLLVAPVQSQSPFLGVAGAPELAKD 441
QY 448 KKLRDVFKKGLDYFNSGDLMLVHDENIYFHDRVGDTRFKNGENAVATEVADTVGLVDVF 507
DB 442 KLLKDVFGSDVFFNTGDLVCDQGLFHFHDTGDTIRWNGENAVATEVAEVLDTDFL 501
QY 508 QEVNIVYGVHPDHEGRIGMASIKMKENHEFDGKKLFQIHADIYLPYSYARPFRLQDPIEI 567
DB 502 QEVNIVYGVHPDHEGRIGMASIKMKENHEFDGKKLFQIHADIYLPYSYARPFRLQDPIEI 567
QY 568 TGTFRHRRMTLVVEGFNPVAVIKDALYFLDDTAKMYVPMTEDIYNAISAKTIKL 620
DB 562 TETFKQKVRMANEGFDPVSLDPLVYLDQDIGAYLPLTPARYSALLSGDLRI 614

RESULT 8
Q9WLV9 ID Q9WLV9 PRELIMINARY; PRT; 671 AA.
AC Q9WLV9;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE CG3037 PROTEIN.
GN CG3037.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacile J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svoboda R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL "The genome sequence of Drosophila melanogaster."

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DR EMBL; AB003459; AAF46943.2; --  
DR FlyBase; FBgn0034812; CG3037.  
DR InterPro; IPR000873; --  
DR Pfam; PF00501; AMP-binding; 1.  
DR PROSITE; PS00455; AMP\_BINDING; 1.  
SQ SEQUENCE 671 AA; 74780 MW; 1816C085F4309514 CRC64;

Query Match 32.1%; Score 1051; DB 5; Length 671;  
Best Local Similarity 39.3%; Pred. No. 1.1e-70;  
Matches 230; Conservative 98; Mismatches 239; Indels 18; Gaps 8;

QY 48 QRRPARTILRAFLKARQTPHKKPFLFRDETLYAQVDRRSNOVARALHDLHGLRQDCV 107  
DB 91 QERKLNIGDIFESNVARQPKLAIYSESQQWTFQVNEHSNRVANVFHSH-GYKKGDDV 149  
QY 108 ALLMGNEPAAVWLGLVLCGACMACLNINRAKSLHFCGCCAKVLLVSPLELAQVEE 167  
DB 150 GLLEHRAEFATWGLSGKIGVITPLINTNLRGASLQHSITVGQCTALYIGASFRSAVMD 209  
QY 168 ILPSLKKDDVSIYVSRSTN-----TDGIDSFLDKVDVSEVTEPIPESEWRSEVTFST 218  
DB 210 IAKDLPA-HVGLYQFNDESQEVASEGLSQGLAQLNGLLETAAKDKVAAGASRADHHD 268  
QY 219 PALYIYTSGTGLPKAMITHORINW-GRGLTFVSGLKADDDVYITLPPYHSAALLIGH 277  
DB 269 KLVYIYTSGTGLPKAAVITHSRIFFAAGIHYTLGFKDQDDVFTPLPLYHTAGVMSMG 328  
QY 278 GCIVAGATIALTKFSASQFDDCRKYNVTQYIGELLRYLCNSPOKPNDRDKVRLAL 337  
DB 329 QALLFGSTVYIRKFSASGIFSDCAEEDTGVQYIGEMARYILATPSAPDRNHQVWF 388  
QY 338 NGNLGRDVMVRQFVKRFGDICIYEFYAEATGEGNFMNARKVAGVGRVNYLQKKIITYDLI 397  
DB 389 NGNLGRQIWPQFVERGIRKVEFYGATEGANINMNDSTVGAIGFISRLPQIYPIISII 448  
QY 398 KYDVEKDEPRDENGVCVRPGKEVGLLVCKITQLTP----FNGYAGAKAQTCKKLRFV 454  
DB 449 KADPHGTGEPLRNSQGLCEADEPGVFVGKVRGNPCREFLGYVDOKA-SSKKVHVDF 507  
QY 455 KKGDLVNSGDLMLVDHFNFIYFHDVRGDTFRKKGNNVATTEVADTVGLVDFVQEVN 514  
DB 508 SKGDMAFISGDLVADBERGLYFKDRTGDTFRKKGNNVSTSEVEAQLSNLAGYKDVYVG 567  
QY 515 VHPDHEGRIGMASIKMENHEPDGKLFQHIADYLPSPARPRFLRQIDTIBITGTFK 574  
DB 568 VSPNTEGRAGMAAI-YDPTRENVNSQLGVELAKSLPNYARQFLRFLRKIDLTGTFKLR 626  
QY 575 KMTLVGEFNPVAKIDALYFLDDTAKMYVPMTEIDIYNAISATLK 619  
DB 627 KVELQQGFNPETIIDELFYAOPDG-VYAPLTPSVYERIVRNELR 670

RESULT 9  
Q9W185 PRELIMINARY; PRT; 661 AA.  
AC Q9W185;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAY-2001 (TREMBLrel. 16, Last annotation update)  
DE CG3394 PROTEIN.  
GN CG3394.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
RA Arif J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhargava P., Boldt R.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Dou L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.-Y., Wasarman D.A., Weinstock G.M., Weissbach J.,  
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
RT "The genome sequence of Drosophila melanogaster.";  
RL Science 287:2185-2195(2000)  
DR EMBL; AE003463; AAF47192.1; --  
DR FlyBase; FBgn0034999; CG3394.  
DR InterPro; IPR000873; --  
DR Pfam; PF00501; AMP-binding; 1.  
DR PROSITE; PS00455; AMP\_BINDING; 1.  
SQ SEQUENCE 661 AA; 73598 MW; DECE2762C438FFC8 CRC64;

Query Match 31.4%; Score 1026; DB 5; Length 661;  
Best Local Similarity 37.9%; Pred. No. 8.1e-69;  
Matches 244; Conservative 112; Mismatches 223; Indels 64; Gaps 17;

QY 3 SAITYVLAGLLFLPLVNLCCPYFFQDIGYFLKVAAGVRVRSYGQR-----R 50  
DB 34 NALASLTGLGAVVALLRN---PTF-----VFALVMTASRDLEAF-QRFVALNYLKKDR 84  
QY 51 PARTILRAFLEKARQTPHKKPFLFRDETLYAQVDRRSNOVARALHDLHGLRQDCVALL 110  
DB 85 GGFTVARCFQDQARRRPPKTCFVMDRHLRSLFAEALEFSQKIAGYFSDR-GLRGDCVALL 143  
QY 111 MGNPAAVWMLGLVLCGACMACLNINRAKSLHFCGCCAKVLLVSPLELAQVEILP 170  
DB 144 METRLEPCWGLSGLQGVITALINSNLGRGSLHSHKIVANAKALIVGSELL-----DVLV 199  
QY 171 SLKK-----DVSIIY-----VSRSTNTDGDIDSLDKVDVSTEP-----IPESWRSE 213  
DB 200 SLRKEQLDEVPYIYQYTDDEVGVAGHDLPLPGAVDLVLTALKTKLELPSAVCPGEARSK 259  
QY 214 VTFSTPALYIYTSGTGLPKAMITHOR-IWYGTGLTFVSGLKADDDVYITLPPYHSAAL 272  
DB 260 L-----LYVYTSGTGLPKAAVITNLREFMSSAGSYMLKSSDDVYDPLLYHTAGG 313  
QY 273 LIGHGIVAGATIALTKFSASQFDDCRKYNVTQYIGELLRYLCNSPOKPNDRDKH 332  
DB 314 IVGVGNAILNGSTVYLRKFKFSARNFWDCCDRHNCVTAQYIGELCRYLLATYSFPDQKH 373  
QY 333 VRLALGNLGRDVMVRQFVKRFGDICIYEFYAEATGEGNFMNARKVAGVGRVNYLQKKII 392



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Db 374 LRLMGNGLRQWQVFRFGPHGEIYGATEGNSNLININRVRGAIGFVPVYGSLLY 433
QY 393 TYDLIKYDEKDFVDRDENGVCYVRPKGEVGLLVCKI---TOLTFFNGYAGAKAOTEKKK 449
Db 434 PQVLRCDVETGELLNDSRGHCIRCPQAGNGLVGVKVDARRASAFHGTAD-KGASEQKL 492
QY 450 LRDFVFKGDDLYFNSSGDLMLVMDHNFYIFHDRVGDTEFRWGENVATTEV---ADTVGLVD 505
Db 493 LRNVFTSGDVFNFSGDMVRDILGYEFKDKTGDTEFRWGENVATTEV---ADTVGLVD 505
QY 506 FVQEVNRYGVHVPDHEGDMASIKMKENHEPDKKLFQHIADYLPYSYARFRLRIQDTI 565
Db 553 CV-----YGVQIPHEGKAGMAI--VDPKRVMDYLSVVLGRSLPPYARPLFRLILDEI 607
QY 566 EITGTFKHKMTLVVEGFPNPAVFKDALYFLDDTAKMYVPWMTD 608
Db 608 PRATEKLAKRELAKAYDIGQSDPYLYNDRG-IYRPLSQE 649

RESULT 10
Q9VRU1 ID Q9VRU1 PRELIMINARY; PRT; 690 AA.
AC Q9VRU1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 16, Last annotation update)
GN FATP OR CG7400.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyrididae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazer J.R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.I., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,

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RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
DR EMBL; AE003629; AAF52969.1; -.
DR FlyBase; FBgn0021953; Fatp.
DR InterPro; IPR000873; -.
DR Pfam; PF00501; AMP-binding.1.
DR PROSITE; PS00455; AMP-BINDING; 1.
SQ SEQUENCE 690 AA; 77541 MW; 3A1B7CCDB104060B CRC64;

Query Match 30.1%; Score 983.5; DB 5; Length 690;
Best Local Similarity 37.4%; Pred. No. 1.4e-65;
Matches 216; Conservative 108; Mismatches 222; Indels 31; Gaps 11;

QY 54 TILRAFLEKARQTHPKFLLPRDETLTYAQVDRRSNOVARALHDLGLRGDCVALLMGN 113
Db 133 TVADVFERNVQHPDKVAVVSETQRTFRQVNEHANKVANVLAQ-GYKKGDVVALLLEN 191
QY 114 EPAYVWLWGLVGLKGCAMACLNYNIRAKSLHCFQCCGAKVLLVSPLOAAVEELPSLK 173
Db 192 RAEYVATWGLSKIGVITPLINTNLRGPSLLHSTVAHCSALIYGEDFLCAVTDVAKDLP 251
QY 174 KDDVSIYVSRSTNVDGIDSLDKVDE----VSTEPIPESWRSEVTEFSPALXIYTSGT 229
Db 252 A-NLTFLQFNENNNSSETEKNIPQAKNLNALLTTASVEKPNKTVNHHDKLVIYTSGT 310
QY 230 GLPKAAVITHOR-IWYGTGLTFVSGLKADDDVIYITLFFYSAALLIGIHCIVAGATLAL 288
Db 311 GLPKAAVISHRYLFIAGIHYTMGFEEDIFVTPLHYTAGGIMCMGOSVLFGSTVSI 370
QY 289 RTKESQFWDCKRYKNVTYQYIGELLRYLNCSPQKN--DRDHKVRALGNGLRGDVW 346
Db 371 RKKEFSASNYFADCAKYNATV-----TTKPEYDQKHVRVLFVFGNGLRQIWI 416
QY 347 RQVFRGDCIYEFYAAETEGNFMNRYKRVAGVRVNYLQKKIITDILIKYDVEKDEP 406
Db 417 PQFYQVRENIAKVGFEYGAETEGNANIMHNDVNTVAIGFVSRILPKIYPIISIRADPDTEP 476
QY 407 VRDENGCVVRPKGEVGLLVCKITQLTTP---FNGYAGAKAOTEKKLRDVFVKGDLYFNS 453
Db 477 IRRNGLCQLCAPNEPGVFIKGVKGNPSREFIYGVDEKA-SAKKIYKDVFKHGMFAFIS 535
QY 464 GDLLMDHNFYIFHDRVGDTEFRWGENVATTEVADTVGLVDFVQEVNRYGVHVPDHEGR 523
Db 536 GDLLVADEKGLYFKDRTGDTFRWGENVSTSEVAQVSNVAGYKDTVYGVITPTEGR 595
QY 524 IGNASIKMKENHEFDGKKLFQHIADYLPYSYARFRLRIQDTIETGTFKHKMTLVVEGF 583
Db 596 AGMAIYDPE-RELDLDVFAASLAKVLPAYARPQIIRLLTKVDLTGTGFKLRKVDLQKEG 654
QY 584 NPAVICKDALYFLDDTAK-MYVPMTEDITYNAISAKTLK 619
Db 655 DPNAIKDALY--QTSKGRIELTTPQYDQVQNEIR 689

RESULT 11
Q19878 ID Q19878 PRELIMINARY; PRT; 650 AA.
AC Q19878;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
GN FATTY ACID TRANSPORTER PROTEIN A (F28D1.9 PROTEIN).
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Baynes C.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.

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-!- FUNCTION: INVOLVED IN TRANSLLOCATION OF LONG-CHAIN FATTY ACIDS (BY SIMILARITY).  
 -!- SIMILARITY: TO OTHER ENZYMES WHICH ACT VIA AN ATP-DEPENDENT COVALENT BINDING OF AMP TO THEIR SUBSTRATE.

EMBL: Z70684; CAA94602.1; -.  
 WormPep; F28D1.9; CE05749.  
 DR InterPro; IPR000873; -.  
 DR Pfam; PF00501; AMP-binding; 1.  
 DR PROSITE; PS00455; AMP-BINDING; 1.  
 KW Glycoprotein; Lipid transport; Transmembrane; Transport.  
 FT TRANSMEM 23 43 POTENTIAL.  
 FT TRANSMEM 137 157 POTENTIAL.  
 FT TRANSMEM 286 306 POTENTIAL.  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 518 518 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 650 AA; 72759 MW; F2D16649EA13288A CRC64;

Query Match 29.3%; Score 958; DB 5; Length 650;  
 Best Local Similarity 38.5%; Pred. No. 1e-63;  
 Matches 222; Conservative 97; Mismatches 225; Indels 32; Gaps 15;

QY 59 FLEKARQTHKPL--LFRDELTITVAQVDRSRNOVARALHDLHGLRQDCVALLMGNEPA 116  
 DB 81 FLDIVKKNPKAMIDIEINTTETAEFAHCHNRANYFQG-LGYRSGDVVALYMSVYE 139  
 QY 117 YVWLGLVKLGKAMACLNINRAKSLHLCFOCGAKVLLVSPQLQ---AAVEELPSL 172  
 DB 140 FVAWGLAKIGVVTAWINSNLRKQOLVHCITASKTALITSVTLQNLMLDAIDQKL--F 197  
 QY 173 KDDVSIIYVSRNTGDSFLDKVD-EVSTPEIPESRSEVTFSTPALYIYTSGLTGL 231  
 DB 198 DVGIEVSYGPEKPKNSGFKNLKKLDAQITTEP---KTLDIVDFKSLICFYTSGLTGM 254  
 QY 232 PKAAMLTTHOR---IWKVGTGLTFVSGLKADDDYITLPLFYHSAALLIGHGCIIVAGATLAL 288  
 DB 255 PKAAVWKHFRIYSIAVGAAKSP--GIRPSDRMVSNPIYHTAAGILGVQALLGSSCVI 312  
 QY 289 RTKFSASQFDDCKRYNVTYQVIGELLYRCLNSPOKPNDRDHKVRALGNLGRDGVWRQ 348  
 DB 313 RKKFSASNFRDCVKYDCTVSQYIGECIRYLLAQPVVEESRHRMRLLVGNGLRAEIQWP 372  
 QY 349 FVKRFQDICIYEFAATEGNIGMNYARKVGAVG--RVNVLQKKIITYDLIKYDVEKDEP 406  
 DB 373 FVDRF-RVRIGELYSGTESSLVNIDGHVGCGLFPISELPKMKHPVRLIKVDVDTGEA 431  
 QY 407 VRDENGVCYVRPKGEYGLLVCKITQLTP---FNGYAGAKAQTEKKKLRDVFKKGLDYNS 463  
 DB 432 IRSDGLCIACNPGESGAMVSTIRKNNPLLQFEGYLN-RKETNKKLIIRDVFAKGSCLFT 490  
 QY 464 GDLMDHNFYIFHDVGDGTFRWKGENVATTEVADTVGLVDFVQEVNYYGVHVPDHEGR 523  
 DB 491 GDLMDHNLGYVFKDRTGDTFRWKGENVSTTEVEAILHPITGLSDATYGVVEVPQREG 550  
 QY 524 IGMAIKMENHEFDGKKLFQH-----IADYLPYSARPRFLRIQDTIEITGTFKHKMPL 578  
 DB 551 VGMASVVRVVSHEED-ETQPVHRVGARLASSLTSYAIPOFMRICODVEKTFGFKLVKTNL 609  
 QY 579 VEEGFNPVAKDALYFLDDTAKMVPMTEDIYNALIS 614  
 DB 610 QRLGIMDAP-SDSIYIYNSNRRNFVPFNDLRCKVS 644

RESULT 12  
 Q9HZV4 PRELIMINARY; PRT; 608 AA.  
 AC Q9HZV4  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE PROBABLE VERY-LONG-CHAIN ACYL-COA SYNTHETASE.  
 GN PA2893.  
 OS, Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=PA01;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 Ra Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 DR EMBL: AE004715; AAG06281.1; -.  
 DR InterPro; IPR000873; -.  
 DR Pfam; PF00501; AMP-binding; 1.  
 DR PROSITE; PS00455; AMP-BINDING; 1.  
 SQ SEQUENCE 608 AA; 67647 MW; D2E134AB8BAD4FF7 CRC64;

Query Match 29.1%; Score 953; DB 2; Length 608;  
 Best Local Similarity 38.1%; Pred. No. 2.2e-63;  
 Matches 222; Conservative 94; Mismatches 210; Indels 56; Gaps 14;

QY 60 LEK-AROTPHKPFELFRDELTITVAQVDRSRNOVARALHDLHGLRQDCVALLMGNEPAY 118  
 DB 48 LERARLPDPNPAYLDGGRISYALFNAGWANRLARAFKAE-GVGHGSVVAAMLENRVELL 106  
 QY 119 WLWGLVKLGKAMACLNINRAKSLHLCFOCGAKVLLVSPQLQAAVEELPSLKKDDVS 178  
 DB 107 AILAAALAKLGAIGALVNTQGRKVLVHSLNLPKGVVEELREVEFEVRHVELGNAGH 166  
 QY 179 IYVYSRTSNTDGDIFSFLDKVDVESTPEIPESWRS-----EYTFSTPAL 221  
 DB 167 CYWD-----DG-----DTLGDGSGPPM--GWRNLMRLAQGTSENLEDTRVRLKDSCF 214  
 QY 222 YIYTSGLTGLPKAMITHQRIW---YG-----TGLTFVSGLKADDDYITLFFHSAALLI 274  
 DB 215 YIYTSGLTGLPKASIMSHGK-WIKAYGGFGHSLG---GLGRDDVLYTLPLCYHNNAVT 269  
 QY 275 GIHGCIVAGATLALRTKFSASQFDDCKRYNVTYQVIGELLYRCLNSPOKPNDRDHKVR 334  
 DB 270 CWSRALAGGAAMALRRFASGFWKDYHYRATCFYIGELCRVLLNQPPCAEERGNLSLT 329  
 QY 335 LALGNLGRDGVWRQVRFKFGDICIYEFYATGEGNIGFMNYARKVGAVGRVNYLQKKIITY 394  
 DB 330 CMIGNLRPSIWAEFKQRFETIRTEFYASSEGNIPTNFNFDTYV-----FSPATY 383  
 QY 395 DLIKYDVEKDEPVDENGCVYRVPKGEVGLLVCKITQLTPNGYAGAKAQTEKKKLRDVF 454  
 DB 384 AIVRYDLNDRPVDAKGFMEKVGKGEVGLLISAKWPFDDGTYD-PAKSEAVILRDVF 442  
 QY 455 KKGOLYFNSGDLIM---VDHENFIYFHDVGDGTFRWKGENVATTEVADTVGLVDFVQEVN 511  
 DB 443 KKGDAWFTGDLMRDIGFKHTQFV---DRLGDTFRWKGENVSTTEVENALGAFDGEDAV 499  
 QY 512 YGVHVPDHEGRIGMASIKMENHEFDGKKLFQHIADYLPYSARPRFLRIQDTIEITGTF 571  
 DB 500 YGVIEPTGTCGMAALRLADGVLEDRDLAAHLDRLEPAYATPVFLRLLEVEYTTGTF 559  
 QY 572 KHRKMTLVEEGFNPVAKDALYFLDDTAKMVPMTEDIYNAL 613  
 DB 560 KYKTDLARDAYDPAFVSDKLFVRLPGSAGYQPLDAELYQAL 601

RESULT 13  
 Q05307 PRELIMINARY; PRT; 597 AA.  
 AC Q05307;  
 DT 01-JUL-1997 (Tremblrel. 04, Created)





[illegible]

Db	184	ITNINLLPMFKAAREK---NLSIDEIHLVFLAG--TQVDGRHRSLOQDLHLFSEDE---PP	235
QY	206	IPESWRSEVTESTPALYIYTSGTGLPKAAMITHOR-IWYGTGLTFVSGLKADDVYITL	264
Db	236	VTDG-----LNPRSLVLCIYVTSGTGNPKPAVKHPRYFWIAMGAKAFGINKSDVVITM	291
QY	265	PFYHSAALLIGHCICIVAGATLALRNKFSASOFWDCRKYNTVIOYIGELLARVLNSPQ	324
Db	292	PMYHSAAGIMIGSLIAFGSTAVIRKKFSRNFWDCKVYNVTATQYIGEICRYLLAANP	351
QY	325	KPNDRDHKVRALONGLURGDWRFQYKRGDICIYEFYAATEGNIGFMNTARKVGAVGRV	384
Db	352	CPEEKQHNVLMMWGLGQIWKFEYRGFGIRKKIGELYGSTEGSNINVDNVHVGACGMF	411
QY	385	NYLQK-KIITYDLIKVDEKDEPDVDENGYCVRPKPEVGLLYCKITQ---LTPPENGVA	439
Db	412	PIYPHIGSLYPVRLIKVDRTAGLERDKNGLCVPCVPGETGEMGVVIXEKDILLKEGYV	471
QY	440	GAKAOTEKKLRVFKFGDGLYFNSGOLLVMQHENIYFPHDRVGTGTFRWKGENVATTEAD	499
Db	472	-SEGDTAKRIYDRFKHGDKVFASGDLHWDGLGLYFVDRCGDTFRWKGENVSTTVEEG	530
QY	500	TVGLVDVFQEVNRYGVHPVDHEGRIGMASTKMKENHEFDGKKLFQHIADY-----LPS	552
Db	531	ILQPWMDVEDATVYGVTVGRMEGRACMAGIVVK-----DGTQDVEKFTADITSRLTENLAS	585
QY	553	YARPFRLQDTIELTCTFFHKRMKTLVESGFNPVNIK-DALYFLDDTAKMYVPMTEDIYN	611
Db	586	YAIYPFIRLCEVDRTGTFKLKLTDLQKQGYDLVACKGDPIYYSAAEKSKYKPLTDKMQQ	645
QY	612	AI	613
Db	646	DI	647

Search completed: July 16, 2001, 18:14:46  
Job time: 187 sec